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EXAMINER	
SWITZER, JULIET CAROLINE	
ART UNIT	**PAPER NUMBER**
1634	

DATE MAILED: 08/23/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/032,260	MERCOLA ET AL.	
	Examiner	Art Unit	
	Juliet C. Switzer	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) 1-31 is/are pending in the application.

4a) Of the above claim(s) 30 and 31 is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) 1-29 is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. Restriction to one of the following inventions is required under 35 U.S.C. 121:

I. Claims 1-29, drawn to methods for isolating nucleic acid fragment comprising at least a portion of a gene, classified in class 435, subclass 6.

II. Claim 30, drawn to a composition having a DNA sequence, classified in class 536, subclass 23.1..

III. Claim 31, drawn to a composition having an amino acid sequence, classified in class 530, subclass 300, for example.

The inventions are distinct, each from the other because of the following reasons:

2. Inventions I, II, and III are unrelated. Inventions are unrelated if it can be shown that they are not disclosed as capable of use together and they have different modes of operation, different functions, or different effects (MPEP § 806.04, MPEP § 808.01). In the instant case the different inventions are unrelated insofar as the methods of invention I do not recite or require the products of inventions II and III. Further, the products of invention II are not related to the products of invention III because one is a nucleic acid (i.e. composed of nucleotides and useful, for example in hybridization assay) and the other is a polypeptide (i.e. composed of amino acids and useful, for example in a fusion protein).

3. During a telephone conversation with David Waller on 7/29/04 a provisional election was made without traverse to prosecute the invention of group I, claims 1-29. Affirmation of this election must be made by applicant in replying to this Office action. Claims 30-31 are

withdrawn from further consideration by the examiner, 37 CFR 1.142(b), as being drawn to a non-elected invention.

4. Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a request under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(i).

Priority

5. This application repeats a substantial portion of prior Application No. 09/270391, filed 3/16/99, and adds and claims additional disclosure not presented in the prior application. Since this application names an inventor or inventors named in the prior application, it may constitute a continuation-in-part of the prior application. Should applicant desire to obtain the benefit of the filing date of the prior application, attention is directed to 35 U.S.C. 120 and 37 CFR 1.78. Applicant is advised that a petition is required in order to add any claim to priority in this application.

Claim Rejections - 35 USC § 102

6. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

7. Claims 1-10 and 20-29 are rejected under 35 U.S.C. 102(b) as being anticipated by de Belle *et al.* (BioTechniques 29: 162-169, July 2000).

With regard to claim 1, de Belle *et al.* teach a method for isolating a nucleic acid molecule fragment comprising a portion of a gene, comprising:

(a) stimulating at least one cell or at least one nucleus with radiation (p. 164, 3rd column);

(b) cross-linking at least one transcription factor to a nucleic acid molecule in said at least one cell or at least one nucleus with formaldehyde, forming at least one transcription factor-nucleic acid molecule complex (p. 163, 1st column; see Figure 1;

(c) fragmenting said nucleic acid molecule to form at least one transcription factor-nucleic acid molecule complex (p. 163, 2nd column);

(d) isolating the nucleic acid molecule fragment from said at least one transcription factor-nucleic acid molecule fragment complex to form at least one isolated nucleic acid molecule fragment (p. 163, 2nd column); wherein said at least one isolated nucleic acid molecule fragment comprises at least a portion of the first exon of a gene whose expression is modulated by said transcription factor (p. 164, 2nd column); further wherein said at least one isolated nucleic acid molecule fragment comprises at least one transcription factor binding site that is operably linked or in close proximity to said first exon of a gene (p. 164, 2nd column; As evidenced by amplification of TGFβ1 promoter from nucleotides -182 through 138).

With regard to claim 2, de Belle *et al.* teach a method for isolating at least one nucleic acid molecule fragment that comprises a portion of a gene regulated by a transcription factor, comprising:

(a) cross-linking at least one transcription factor to at least one nucleic acid molecule in at least one cell or at least one nucleus, forming at least one transcription factor-nucleic acid molecule complex (p. 163, 1st column; see Figure 1;

(b) fragmenting said nucleic acid molecule to form at least one transcription factor-nucleic acid molecule complex (p. 163, 2nd column); and

(c) isolating the nucleic acid molecule fragment from said at least one transcription factor-nucleic acid molecule fragment complex to form at least one isolated nucleic acid molecule fragment (p. 163, 2nd column);

wherein said at least one isolated nucleic acid molecule fragment comprises at least a portion of the first exon of a gene whose expression is modulated by said transcription factor (p. 164, 2nd column); further wherein said at least one isolated nucleic acid molecule fragment comprises at least one transcription factor binding site that is operably linked or in close proximity to said first exon of a gene (p. 164, 2nd column; As evidenced by amplification of TGFβ1 promoter from nucleotides -182 through 138).

With regard to claim 3, de Belle *et al.* isolated the nucleic acid fragment from genomic DNA (p. 163).

With regard to claims 4 and 5, the transcription factor is Egr-1 which is a Cys2His2 zinc finger factor.

With regard to claim 6 and 7, de Belle *et al.* use cells and the cells are living cells (p. 163, 1st column).

With regard to claim 8, the cells are irradiated prior to cross-linking (p. 164, 2nd column).

With regard to claim 9, the cross-linking is performed using formaldehyde (Figure 1).

With regard to claim 10, de Belle *et al.* further teach amplifying the fragments (p. 163, 3rd column).

With regard to claim 20, de Belle *et al.* teach a method for isolating one or more genes or DNA sequences regulated by a transcription factor comprising:

(a) cross-linking at least one transcription factor to at least one nucleic acid molecule in at least one cell or at least one nucleus, forming one or more transcription factor-nucleic acid molecule complex (p. 163, 1st column; see Figure 1);

(b) fragmenting said at least one nucleic acid molecule to form one or more transcription factor-nucleic acid molecule complex (p. 163, 2nd column); and

(c) isolating one or more nucleic acid molecule fragments from said at least one or more transcription factor-nucleic acid molecule fragment complexes to obtain at least one or more isolated nucleic acid molecule fragments (p. 163, 2nd column);

(d) hybridizing said one or more isolated nucleic acid fragments to a known complementary nucleic acid sequence in an array of sequences known to be complementary to previously identified nucleic acid molecules of known sequence (¶ bridging p. 163-164); and identifying one or more genes of DNA sequences regulated by a transcription factor when said one or more genes or DNA sequences regulated by a transcription factor hybridizes to one or more isolated nucleic acid fragments on said array.

With regard to claim 21, de Belle *et al.* teach amplifying the isolated nucleic acid molecule fragments prior to identification (p. 163, 3rd column; Figure 1).

With regard to claim 22, de Belle *et al.* isolated the nucleic acid fragment from genomic DNA (p. 163).

With regard to claims 23, 24, and 25, the transcription factor is Egr-1 which is a Cys2His2 zinc finger factor.

With regard to claim 26 and 27, de Belle *et al.* use cells and the cells are living cells (p. 163, 1st column).

With regard to claim 28, the cells are irradiated prior to cross-linking (p. 164, 2nd column).

With regard to claim 29, the cross-linking is performed using formaldehyde (Figure 1).

8. Claims 2, 3, 6, 7, 9, 10, 20, 21, 22, 23, 26,, 27, and 29 are rejected under 35 U.S.C. 102(b) as being anticipated by Orlando *et al.* (Cell, Vol. 75, 1187-1198, December 1993).

With regard to claim 2, Orlando *et al.* teach a method for isolating at least one nucleic acid molecule fragment that comprises a portion of a gene regulated by a transcription factor, comprising:

(a) cross-linking at least one transcription factor to at least one nucleic acid molecule in at least one cell or at least one nucleus, forming at least one transcription factor-nucleic acid molecule complex (p. 1195, Experimental Procedures, Cells, Labeling, and Formaldehyde Fixation);

(b) fragmenting said nucleic acid molecule to form at least one transcription factor-nucleic acid molecule complex (p. 1196, first column); and

(c) isolating the nucleic acid molecule fragment from said at least one transcription factor-nucleic acid molecule fragment complex to form at least one isolated nucleic acid molecule fragment (p. 1196, first column);

wherein said at least one isolated nucleic acid molecule fragment comprises at least a portion of the first exon of a gene whose expression is modulated by said transcription factor; further wherein said at least one isolated nucleic acid molecule fragment comprises at least one transcription factor binding site that is operably linked or in close proximity to said first exon of a gene (p. 1189-1190; see especially Figure 4 legend teaching that the decross-linked DNA fragment cover the transcriptional start site of the Antp-P1 promoter region).

With regard to claim 3, Orlando *et al.* isolated the nucleic acid fragment from genomic DNA (p. 1195, Experimental Procedures, Cells, Labeling, and Formaldehyde Fixation).

With regard to claim 6 and 7, Orlando *et al.* use cells and the cells are living cells (p. 1195, Experimental Procedures, Cells, Labeling, and Formaldehyde Fixation).

With regard to claim 9, the cross-linking is performed using formaldehyde (p. 1195, Experimental Procedures, Cells, Labeling, and Formaldehyde Fixation).

With regard to claim 10, Orlando *et al.* further teach amplifying the fragments (p. 1196, 1st column).

Orlando *et al.* teach the use of formaldehyde cross-linking in vivo to study the binding of the transcription factor Pc. Pc is considered to be a transcription factor within the scope of the invention because it is involved in transcriptional repression. The specification defines a "transcription factor" as "a molecule that can modulate the expression or transcription of a gene or nucleic acid sequence (p. 16, start of second full ¶)." Thus, because of its role in gene silencing, the protein studied by Orlando *et al.* is a transcription factor.

With regard to claim 20, Orlando *et al.* teach a method for isolating one or more genes or DNA sequences regulated by a transcription factor comprising:

(a) cross-linking at least one transcription factor to at least one nucleic acid molecule in at least one cell or at least one nucleus, forming one or more transcription factor-nucleic acid molecule complex (p. 1195, Experimental Procedures, Cells, Labeling, and Formaldehyde Fixation);

(b) fragmenting said at least one nucleic acid molecule to form one or more transcription factor-nucleic acid molecule complex (p. 1196, first column); and

(c) isolating one or more nucleic acid molecule fragments from said at least one or more transcription factor-nucleic acid molecule fragment complexes to obtain at least one or more isolated nucleic acid molecule fragments (p. 1196, first column);

(d) hybridizing said one or more isolated nucleic acid fragments to a known complementary nucleic acid sequence in an array of sequences known to be complementary to previously identified nucleic acid molecules of known sequence (p. 1189-1190; see especially Figure 4 legend teaching that the decross-linked DNA fragment cover the transcriptional start site of the Antp-P1 promoter region); and

identifying one or more genes of DNA sequences regulated by a transcription factor when said one or more genes or DNA sequences regulated by a transcription factor hybridizes to one or more isolated nucleic acid fragments on said array (p. 1189-1190; see especially Figure 4 legend teaching that the decross-linked DNA fragment cover the transcriptional start site of the Antp-P1 promoter region).

With regard to step (d) of claim 20, Orlando *et al.* teach that the isolated fragments were hybridized to eight partially overlapping fragments of the pATP 1.o clone that covers the Antp-P1 start site. Thus, Orlando *et al.* teach hybridizing the fragments to a known complementary

sequence in an array of sequences and identifying the sequences regulated by Pc when hybridization occurs.

With regard to claim 21, Orlando *et al.* teach amplifying the isolated nucleic acid molecule fragments prior to identification (p. 1189 and 1196).

With regard to claim 22, Orlando *et al.* isolated the nucleic acid fragment from genomic DNA (p. 1195).

With regard to claim 26 and 27, Orlando *et al.* use cells and the cells are living cells (p. 11195).

With regard to claim 29, the cross-linking is performed using formaldehyde (p. 1195).

Claim Rejections - 35 USC § 103

9. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

10. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

11. Claims 1, 4, 5, 8, 24, 25, and 28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Orlando *et al.* in view of Hallahan *et al.* (The Journal of Biological Chemistry, Vol. 270, No. 51, p. 30303-30309).

With regard to claim 1 and claims 4, 5, and 8, Orlando *et al.* teach a method for isolating at least one nucleic acid molecule fragment that comprises a portion of a gene regulated by a transcription factor, comprising:

(a) cross-linking at least one transcription factor to at least one nucleic acid molecule in at least one cell or at least one nucleus, forming at least one transcription factor-nucleic acid molecule complex (p. 1195, Experimental Procedures, Cells, Labeling, and Formaldehyde Fixation);

(b) fragmenting said nucleic acid molecule to form at least one transcription factor-nucleic acid molecule complex (p. 1196, first column); and

(c) isolating the nucleic acid molecule fragment from said at least one transcription factor-nucleic acid molecule fragment complex to form at least one isolated nucleic acid molecule fragment (p. 1196, first column);

wherein said at least one isolated nucleic acid molecule fragment comprises at least a portion of the first exon of a gene whose expression is modulated by said transcription factor; further wherein said at least one isolated nucleic acid molecule fragment comprises at least one transcription factor binding site that is operably linked or in close proximity to said first exon of a gene (p. 1189-1190; see especially Figure 4 legend teaching that the decross-linked DNA fragment cover the transcriptional start site of the Antp-P1 promoter region).

Orlando *et al.* teach that the cross-linking is carried out using formaldehyde (p. 1195).

With regard to claims 24, 25, and 28, Orlando *et al.* teach a method for isolating one or more genes or DNA sequences regulated by a transcription factor comprising:

(a) cross-linking at least one transcription factor to at least one nucleic acid molecule in at least one cell or at least one nucleus, forming one or more transcription factor-nucleic acid molecule complex (p. 1195, Experimental Procedures, Cells, Labeling, and Formaldehyde Fixation);

(b) fragmenting said at least one nucleic acid molecule to form one or more transcription factor-nucleic acid molecule complex (p. 1196, first column); and

(c) isolating one or more nucleic acid molecule fragments from said at least one or more transcription factor-nucleic acid molecule fragment complexes to obtain at least one or more isolated nucleic acid molecule fragments (p. 1196, first column);

(d) hybridizing said one or more isolated nucleic acid fragments to a known complementary nucleic acid sequence in an array of sequences known to be complementary to previously identified nucleic acid molecules of known sequence (p. 1189-1190; see especially Figure 4 legend teaching that the decross-linked DNA fragment cover the transcriptional start site of the Antp-P1 promoter region); and

identifying one or more genes of DNA sequences regulated by a transcription factor when said one or more genes or DNA sequences regulated by a transcription factor hybridizes to one or more isolated nucleic acid fragments on said array (p. 1189-1190; see especially Figure 4 legend teaching that the decross-linked DNA fragment cover the transcriptional start site of the Antp-P1 promoter region).

With regard to step (d) of claims 24, 25, and 28, Orlando *et al.* teach that the isolated fragments were hybridized to eight partially overlapping fragments of the pATP 1.o clone that covers the Antp-P1 start site. Thus, Orlando *et al.* teach hybridizing the fragments to a known complementary sequence in an array of sequences and identifying the sequences regulated by Pc when hybridization occurs.

With regard to claims 1, 8, and 28 Orlando *et al.* do not teach a step of stimulating at least one cell or nucleus with radiation.

With regard to claims 4, 5, 24, and 25 Orlando *et al.* do not teach methods in which the transcription factor is selected from the group listed in claim 4 or wherein the transcription factor is Egr-1.

Further, Orlando *et al.* teach that the method will be generally applicable to the study of other binding proteins, that the cross-link allows very stringent washing conditions which results in dramatically improved signal to noise ratios, and that the method "should open the way to the identification of in vivo target genes of low abundance transcription factors (p. 1194, ¶ bridging columns).

Orlando *et al.* do not exemplify the method in use with additional transcription factors.

Hallahan *et al.* teach that the Erg-1 is a transcription factor that is implicated in the response of cells to a variety of stressful stimuli, and that the exposure of mammalian cells to ionizing radiation results in the induction of the transcription factor Egr-1 (p. 30303).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have modified the methods taught by Orlando *et al.* so as to have applied the method for the identification of in vivo target genes of the transcription factor Egr-1. One

would have been motivated to make such a modification by the teachings of Orlando *et al.* who teach that their method can be applied for this precise purpose, and by the teachings of Hallahan *et al.* that Erg-1 is a known transcription factor. Further, in such a method one would have been motivated by the teachings of Hallahan *et al.* to have included a step of treating the cells with ionizing radiation prior to cross-linking in order to have induced production of the Erg-1 transcription factor for study. Thus, in view of the teachings of the prior art, the claimed invention is prima facie obvious.

Double Patenting

12. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

13. Claims 1-29 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-9 of U.S. Patent No. 6410233 (herein referred to as the '233 patent). Although the conflicting claims are not identical, they are not patentably distinct from each other because the methods taught in the '233 patent claims are a species of the claimed invention or recite all of the limitations of the instantly claimed invention and therefore anticipate or render obvious the claimed invention. With regard to requirements of claims 1 and 2 that the fragments comprise "at least a portion of a the first exon of a gene whose expression is

modulated by said transcription factor; further wherein said at least one isolated nucleic acid fragment comprises at least one transcription factor binding site that is operably linked or in close proximity to said first exon of a gene," the claims of the '233 patent do not specifically mention this feature, but would inherently result in the isolation of such molecules, particularly with regard to claim 5 which requires that the method of claim 1 is practiced with Egr-1 which binds closely to the transcription start site of genes such as TNF-alpha. Further, with regard to claim 1, for example, the claims of the '233 patent do not teach a single method which has (a) a step of stimulating with radiation, and (b) a step of cross-linking with formaldehyde. However, the claims of the '233 patent include both of these steps (see claims 8 and 9 therein). It would have been prima facie obvious to have practice both of these method steps in a single invention since they are both claimed embodiments of the '233 patent and therefore on their face considered desirable steps in view of the claims in the '233 patent. Therefore, the practice of the methods of claims 1-9 of the '233 patent anticipates or makes obvious the practice of instant claims 1-29.

Claim Objections

14. Claims 1, 2, and 11 are objected to because of the following informalities:

(a) In claim 1, there are two steps labeled "b" and no step "c." This appears to be a typographical error.

(b) There is not proper agreement between the "at least one" and the plural "fragments" in the phrase "at least one ...fragments" in the preamble of claim 2.

(c) There word "fragment" in line 2 of step (e) of claim 11 should be plural to agree with "said one or more" that modifies the fragments.

Appropriate correction is required.

Conclusion

15. Claims 11-19 are free of the prior art. The prior art does not teach or suggest a method in which the amplifying of step (e) is completed "using said one or more nucleic acid molecule fragments as primers to obtain one or more isolated cDNA molecules."

16. No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Juliet C Switzer whose telephone number is (571) 272-0753. The examiner can normally be reached on Monday through Friday, from 9:00 AM until 4:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached by calling (571) 272-0782.

The fax phone numbers for the organization where this application or proceeding is assigned are (703) 872-9306. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (571)272-0507.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of

the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Juliet C. Switzer
Examiner
Art Unit 1634

August 17, 2004